OS-90
0322
#42

OIPE

```
RAW SEQUENCE LISTING              DATE: 03/26/2002
PATENT APPLICATION:  US/10/033,109     TIME: 09:33:25

Input Set : N:\Crf3\RULE60\10033109.raw
Output Set: N:\CRF3\03262002\J033109.raw
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     1 <110> APPLICANT: Allen, Stephen M.
     2         Rafalski, J. Antoni
     3         Sakai, Hajime
     4 <120> TITLE OF INVENTION: Nitrogen Transport Metabolism
     5 <130> FILE REFERENCE: BB-1210
     6 <140> CURRENT APPLICATION NUMBER: 10/033,109
     7 <141> CURRENT FILING DATE: 2001-12-28
    10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
    13 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
W--> 14 <151> PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
    15 <160> NUMBER OF SEQ ID NOS: 14
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    19 <211> LENGTH: 1037
    20 <212> TYPE: DNA
    21 <213> ORGANISM: Zea mays
    22 <400> SEQUENCE: 1
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    24      tctgcgggtt cgtgtccgcg tgggtgctca tcggcgccaa cgccctcgcg gcgcgcttca   120
    25      ggttcgacga cccgctggag gcggcgcagc tgcacggccgg gtgtggcgcc tgggcgtcc   180
    26      tcttcacggg gctcttcgcg gacggcgaaagt acgtggagga gatctacggc gccgggaggc   240
    27      cctacgggct gttcatgggc ggcggcggga agctcctcgc cgcgcagatc atccagatcc   300
    28      tggtgatcgc cgggtgggtg agctgcacca tgggcccgct cttctacgcg ctcaagaagc   360
    29      tgggcctgct gcgcatctcg gccgacgacg agatgtccgg catggacctg acccggcacg   420
    30      gcggcttcgc ctacgtctac cacgacgagg accctggcca caaggccggg gttggtgggt   480
    31      tcatgctcaa gtccgcgcag aaccgtgtcg agccggcggc ggcggtggcg gcggcgacca   540
    32      gcagccaggt gtaaaaaaaa aatcaggaac aaattgaaac cgagctgaag ttacgtgctt   600
    33      gccttttttca gtatgttgtc gcgtatcacg tttgaggtgg atcgtatctg ccggtcagta   660
    34      cgcagtgttt gggcaaatac ttggctactt gggagtcgca agaaattgtg taaattatat   720
    35      agaggaggat ggcgacgaag cacgcatgtg ttacgtagtt ggggtttgtg tgcacatggt   780
    36      ggtgggcagg ggctaggaga gggtttatct ttaggttatt ttcgtagtgg aatgaatctt   840
    37      atgatcggat atccatcgtc ggaaggtgtg gcgggctgct ggtcaagata ggtggcttct   900
    38      atgactatga ggattgaaac aacaagtgga cgattctgtc ctgtggtcac tgctcatcat   960
    39      ccaatctagc ggctttgacg gtcgtgcctt tttagtatca ataatattat tccaagttta  1020
    40      aaaaaaaaaa aaaaaaa                                                  1037
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    43 <211> LENGTH: 183
    44 <212> TYPE: PRT
    45 <213> ORGANISM: Zea mays
    46 <400> SEQUENCE: 2
    47      Thr Arg Phe Ala Ala Ile Thr Ala Gly Cys Ser Val Val Glu Pro Trp
    48       1               5                   10                  15
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Input Set : N:\Crf3\RULE60\10033109.raw
Output Set: N:\CRF3\03262002\J033109.raw

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49      Ala Ala Val Ile Cys Gly Phe Val Ser Ala Trp Val Leu Ile Gly Ala
50                          20                  25                  30
51      Asn Ala Leu Ala Ala Arg Phe Arg Phe Asp Asp Pro Leu Glu Ala Ala
52                      35                  40                  45
53      Gln Leu His Gly Gly Cys Gly Ala Trp Gly Val Leu Phe Thr Gly Leu
54                  50                  55                  60
55      Phe Ala Arg Arg Lys Tyr Val Glu Glu Ile Tyr Gly Ala Gly Arg Pro
56          65                  70                  75                  80
57      Tyr Gly Leu Phe Met Gly Gly Gly Gly Lys Leu Leu Ala Ala Gln Ile
58                      85                  90                  95
59      Ile Gln Ile Leu Val Ile Ala Gly Trp Val Ser Cys Thr Met Gly Pro
60                  100                 105                 110
61      Leu Phe Tyr Ala Leu Lys Lys Leu Gly Leu Leu Arg Ile Ser Ala Asp
62                  115                 120                 125
63      Asp Glu Met Ser Gly Met Asp Leu Thr Arg His Gly Gly Phe Ala Tyr
64          130                 135                 140
65      Val Tyr His Asp Glu Asp Pro Gly Asp Lys Ala Gly Val Gly Gly Phe
66          145                 150                 155                 160
67      Met Leu Lys Ser Ala Gln Asn Arg Val Glu Pro Ala Ala Ala Val Ala
68                  165                 170                 175
69      Ala Ala Thr Ser Ser Gln Val
70                  180
72  <210> SEQ ID NO: 3
73  <211> LENGTH: 1706
74  <212> TYPE: DNA
75  <213> ORGANISM: Glycine max
76  <400> SEQUENCE: 3
77      gcacgagcac tcccaacccc cacccgtagt ttctaccacc ttcagtcacg gcgtaataca    60
78      ctaaccaacc caccatgtcg ctgcctgctt gtcccgccga acaactggcc caacttctcg   120
79      gcccaaacac cacagacgcc tccgccgccg cctcccttat ctgcggccat ttcgcgcgcg   180
80      tggacagcaa gttcgtcgac acggccttcg ccgtcgacaa cacctacctc ctcttttccg   240
81      cctacctcgt tttttctatg cagctcggct tcgccatgct ctgcgccggc tccgtccgcg   300
82      ccaagaacac catgaacatc atgctcaaca acgtcctgga cgctgccgcc gcggcctct    360
83      tctactacct cttcggcttc gccttcgctt tcggctcccc ctccaacgc ttcatcggta   420
84      aacattctt cggcctcaag gacatccctt catcctccta cgactacagc tacttcctct    480
85      accaatgggc cttcgccatc gccgcgcgcg gcatcaccag cggaagcatc gccgaacgca   540
86      cacagttcgt ggcctatctc atctactcct cctctcttcac cggcttcgtc tatccggtgg   600
87      tctcccactg gttctggtcc ccagacggct ggcctctgc ctttaagatc accgaccggc   660
88      tattttccac cggcgtaata gacttcgccg gttccggcgt agtccacatg gtcggcggaa   720
89      tagccggcct atggggagcg ctgatcgaag gcccaagaat gggacgtttc gatcatgcag   780
90      gacgagctgt ggccttgcga ggccacagcg cgtccttagt agtcctggga accttcttgc   840
91      tttggttcgg ttggtacgga tttaaccccg gttcatttaa caaaatccta cttacttacg   900
92      gtaactcagg aaattactac ggtcaatgga gcgcggttgg cagaaccgcg gtcaccacta   960
93      ccctagcggg gtcaacagct gccttgacca cgctattcgg taaacgggtg atatccggtc  1020
94      actggaacgt gaccgatgtc tgcaacgggc tgttaggcgg tttcgccgac ataacagccc  1080
95      gttgctccgt ggttgagcca tgggcagcca tcgtatgcgg tttttgttgct tctatagtat  1140
96      taatagcttg caacaaatta gcagagaagg ttaagttcga cgatcctctg gagggcggcc  1200
97      agttgcacgg tgggtgtggc acgtgggggg tgatattcac ggcgttgttc gcaaaaaagg  1260
98      agtatgtgaa ggaggtttac gggttgggga gggcgcacgg gttgctcatg gggggtggtg  1320
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RAW SEQUENCE LISTING   DATE: 03/26/2002
PATENT APPLICATION: US/10/033,109   TIME: 09:33:25

Input Set: N:\Crf3\RULE60\10033109.raw
Output Set: N:\CRF3\03262002\J033109.raw

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100     ccatgggacc cttgttttgg gggttgaata aactgaagct gttgaggatt tcttcagagg 1440
101     atgagcttgc ggggatggac atgactcgcc atggaggctt tgcttatgct tatgaggatg 1500
102     atgagacgca caagcatggg atgcagttga ggagggttgg gcccaacgcg tcttccacac 1560
103     ccaccactga tgaatgatct tttttttccca tatgcatgtc tcattagtca aacattaaaa 1620
104     ttggatacat attccttgta aggattcaaa ccttggttac ttgttacttc tgttaaaaaa 1680
105     aaaaaaaaaa aaaaaaaaaa aaaaa                                      1706
107 <210> SEQ ID NO: 4
108 <211> LENGTH: 500
109 <212> TYPE: PRT
110 <213> ORGANISM: Glycine max
111 <400> SEQUENCE: 4
112     Met Ser Leu Pro Ala Cys Pro Ala Glu Gln Leu Ala Gln Leu Leu Gly
113     1               5                   10                  15
114     Pro Asn Thr Thr Asp Ala Ser Ala Ala Ala Ser Leu Ile Cys Gly His
115                 20                  25                  30
116     Phe Ala Ala Val Asp Ser Lys Phe Val Asp Thr Ala Phe Ala Val Asp
117             35                  40                  45
118     Asn Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe Ser Met Gln Leu
119         50                  55                  60
120     Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala Lys Asn Thr Met
121     65                  70                  75                  80
122     Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala Gly Gly Leu Phe
123                     85                  90                  95
124     Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Ser Pro Ser Asn Gly
125                 100                 105                 110
126     Phe Ile Gly Lys His Phe Phe Gly Leu Lys Asp Ile Pro Ser Ser Ser
127             115                 120                 125
128     Tyr Asp Tyr Ser Tyr Phe Leu Tyr Gln Trp Ala Phe Ala Ile Ala Ala
129         130                 135                 140
130     Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr Gln Phe Val Ala
131     145                 150                 155                 160
132     Tyr Leu Ile Tyr Ser Ser Phe Leu Thr Gly Phe Val Tyr Pro Val Val
133                     165                 170                 175
134     Ser His Trp Phe Trp Ser Pro Asp Gly Trp Ala Ser Ala Phe Lys Ile
135                 180                 185                 190
136     Thr Asp Arg Leu Phe Ser Thr Gly Val Ile Asp Ala Gly Ser Gly
137             195                 200                 205
138     Val Val His Met Val Gly Gly Ile Ala Gly Leu Trp Gly Ala Leu Ile
139         210                 215                 220
140     Glu Gly Pro Arg Met Gly Arg Phe Asp His Ala Gly Arg Ala Val Ala
141     225                 230                 235                 240
142     Leu Arg Gly His Ser Ala Ser Leu Val Val Leu Gly Thr Phe Leu Leu
143                     245                 250                 255
144     Trp Phe Gly Trp Tyr Gly Phe Asn Pro Gly Ser Phe Asn Lys Ile Leu
145                 260                 265                 270
146     Leu Thr Tyr Gly Asn Ser Gly Asn Tyr Tyr Gly Gln Trp Ser Ala Val
147             275                 280                 285
148     Gly Arg Thr Ala Val Thr Thr Thr Leu Ala Gly Ser Thr Ala Ala Leu
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149                 290                     295                     300
150     Thr Thr Leu Phe Gly Lys Arg Val Ile Ser Gly His Trp Asn Val Thr
151     305                     310                     315                     320
152     Asp Val Cys Asn Gly Leu Leu Gly Gly Phe Ala Ala Ile Thr Ala Gly
153                     325                     330                     335
154     Cys Ser Val Val Glu Pro Trp Ala Ala Ile Val Cys Gly Phe Val Ala
155                     340                     345                     350
156     Ser Ile Val Leu Ile Ala Cys Asn Lys Ser Leu Ala Glu Lys Val Lys Phe
157                 355                     360                     365
158     Asp Asp Pro Leu Glu Ala Ala Gln Leu His Gly Gly Cys Gly Thr Trp
159                 370                     375                     380
160     Gly Val Ile Phe Thr Ala Leu Phe Ala Lys Lys Glu Tyr Val Lys Glu
161     385                     390                     395                     400
162     Val Tyr Gly Leu Gly Arg Ala His Gly Leu Met Gly Gly Gly Gly
163                     405                     410                     415
164     Lys Leu Leu Ala Ala His Val Ile Gln Ile Leu Val Ile Ala Gly Trp
165                 420                     425                     430
166     Val Ser Ala Thr Met Gly Pro Leu Phe Trp Gly Leu Asn Lys Leu Lys
167                 435                     440                     445
168     Leu Leu Arg Ile Ser Ser Gly Asp Glu Leu Ala Gly Met Asp Met Thr
169                 450                     455                     460
170     Arg His Gly Gly Phe Ala Tyr Ala Tyr Glu Asp Glu Thr His Lys
171     465                     470                     475                     480
172     His Gly Met Gln Leu Arg Arg Val Gly Pro Asn Ala Ser Ser Thr Pro
173                     485                     490                     495
174     Thr Thr Asp Glu
175                     500
177 <210> SEQ ID NO: 5
178 <211> LENGTH: 1991
179 <212> TYPE: DNA
180 <213> ORGANISM: Triticum aestivum
181 <400> SEQUENCE: 5
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183     cgccgcggag atgtcggcga cgtgcgcggc ggacctgggg ccgctgctgg gggcggcggc     120
184     ggcgaacgcc acggactacc tgtgcaacag gttcgccgac accacgtccg cggtggactc     180
185     cacctacctg ctcttctcgg cctacctcgt cttcgccatg cagctcggct tcgccatgct     240
186     ctgcgccggc tccgtccggg ccaagaacac catgaacatc atgctcacca acgtgctcga     300
187     cgccgccgcc ggcgcgctct tctactacct cttcggcttc gccttcgcct tcgggacgcc     360
188     gtcgaacggc ttcatcggga agcacttctt cggcctcaag gacatgccgc agaccggctt     420
189     cgactacagc ttcttcctct tccagtgggc cttcgccatc gccgccgccg gcatccacctc     480
190     cggctccatc gccgagagga cgcagttcgt cgcgtatctc atctactcgg ccttccttac     540
191     gggattcgtc tacccggtcg tgtcccactg gatctggtcc gtcgacggct gggcctccgc     600
192     ggcccgcacg tccggcccgc tgctcttcaa gtccggcgtg atcgacttcg ccggctccgg     660
193     cgtcgtgcac atggtcggcg gcatcgcccg cttctggggc gcgctcatcg agggcccccg     720
194     catcggccgg ttcgaccacg ccggccgctc ggtggcgctc aagggccaca gcgcgtcgct     780
195     cgtcgtgctg gggaccttcc tgctctggtt cggctggtac gggttcaacc cggggtcctt     840
196     cgtcaccatc ctcaagtcgt acggcccgcc cgggagcatc aacgggcagt ggtcgggcgt     900
197     gggccgcacc gccgtcgacga cgacgctggc gggcagcgtg gcggcgctca cgacgctgtt     960
198     cgggaagcgg ctccagacgg ggcactggaa cgtggtggac gtctgcaacg gcctgctcgg    1020
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/033,109

DATE: 03/26/2002
TIME: 09:33:26

Input Set : N:\Crf3\RULE60\10033109.raw
Output Set: N:\CRF3\03262002\J033109.raw

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200     cggcttcgtc tccgcctggg tgctcatcgg gctcaacgcg ctcgccggcc gcctcaagta 1140
201     cgacgacccg ctggaggcgg cgcagctgca cggcggctgc ggcgcgtggg ggatcatctt 1200
202     cacggcgctg ttcgccaaga agcagtacgt ggaggagatc tacggcgccg gcaggccgta 1260
203     cgggctgttc ctgggcggcg gcgggcggct gctggcggcg cacatcgtgc agatcctcgt 1320
204     catcgccggc ttcgtgagct gcaccatggg cccgctcttc ttggcgctca agaagctggg 1380
205     cctgctccgc atctcggccg aggacgagat ggacggcatg gacctgaccc ggcacggtgg 1440
206     gttcgcctac gtctaccacg acgacgacga gcacgacaag tcggtcggcg gcttcatgct 1500
207     caggtcggcg cagacccgcg tcgagccggc ggcggcggcg aacagccagg tctaaccaat 1560
208     caagccggac tacgtaacaa gaaatccagt ggaaatcgcc tttctgttct cgcgcgtcat 1620
209     atcacatatg tgatccgatc atgggatcaa tatttccggt gctgtttggg ccaatacttt 1680
210     ggcgctcttg tgttcgttca caagattgta aaattattac actaggacga ggttattttt 1740
211     tttacctttt ttgtgtacat gcgtgcgttt agaggagatg tgtggtgtgt ggatggaatc 1800
212     tgcagggctg gggtttttc tttcttggtg atatcttgtc attttgtggg tggaattttg 1860
213     tgatcatgag ggtgtggtca agataggtgg ctgctcaagg ttgaattgtt gagatttgtc 1920
214     ctctagtacg ggccaccctc tctatcaaaa ctttggcgcg ttttctcgat cgaaaaaaaa 1980
215     aaaaaaaaaa a                                                      1991
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217 <210> SEQ ID NO: 6
218 <211> LENGTH: 494
219 <212> TYPE: PRT
220 <213> ORGANISM: Triticum aestivum
221 <400> SEQUENCE: 6

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223      1               5                  10                  15
224     Ala Ala Asn Ala Thr Asp Tyr Leu Cys Asn Arg Phe Ala Asp Thr Thr
225                     20                  25                  30
226     Ser Ala Val Asp Ser Thr Tyr Leu Leu Phe Ser Ala Tyr Leu Val Phe
227                 35                  40                  45
228     Ala Met Gln Leu Gly Phe Ala Met Leu Cys Ala Gly Ser Val Arg Ala
229             50                  55                  60
230     Lys Asn Thr Met Asn Ile Met Leu Thr Asn Val Leu Asp Ala Ala Ala
231      65                  70                  75                  80
232     Gly Ala Leu Phe Tyr Tyr Leu Phe Gly Phe Ala Phe Ala Phe Gly Thr
233                     85                  90                  95
234     Pro Ser Asn Gly Phe Ile Gly Lys His Phe Phe Gly Leu Lys Asp Met
235                     100                 105                 110
236     Pro Gln Thr Gly Phe Asp Tyr Ser Phe Phe Leu Phe Gln Trp Ala Phe
237                 115                 120                 125
238     Ala Ile Ala Ala Ala Gly Ile Thr Ser Gly Ser Ile Ala Glu Arg Thr
239             130                 135                 140
240     Gln Phe Val Ala Tyr Leu Ile Tyr Ser Ala Phe Leu Thr Gly Phe Val
241     145                 150                 155                 160
242     Tyr Pro Val Val Ser His Trp Ile Trp Ser Val Asp Gly Trp Ala Ser
243                     165                 170                 175
244     Ala Ala Arg Thr Ser Gly Pro Leu Leu Phe Lys Ser Gly Val Ile Asp
245                 180                 185                 190
246     Phe Ala Gly Ser Gly Val Val His Met Val Gly Gly Ile Ala Gly Phe
247                 195                 200                 205
248     Trp Gly Ala Leu Ile Glu Gly Pro Arg Ile Gly Arg Phe Asp His Ala
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VERIFICATION SUMMARY   DATE: 03/26/2002
PATENT APPLICATION: US/10/033,109   TIME: 09:33:27

Input Set : N:\Crf3\RULE60\10033109.raw
Output Set: N:\CRF3\03262002\J033109.raw

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L:14  M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:314 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:318 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:319 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:320 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
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